Bertoglio.

CRF Errors Corrected by the STIC System Branch.

re-rur
9/8/2003

Serial Number: 09/508,745

CRF Processing Date: 9/8/2003
Edited by: ___
Verified by: _____ (STIC staff)

ENTERED

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:

_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:

_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:

☑ Deleted: ☑ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____.

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:

_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:

_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:

_____

_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

1600

```
 3 <110> APPLICANT: Cory, Suzanne
 4        Adams, Jerry
 5        Print, Cris
 6        Gibson, Leonie
 7        Koentgen, Frank
 9 <120> TITLE OF INVENTION: A METHOD OF TREATMENT AND AN ANIMAL MODEL USEFUL FOR
10        SAME
12 <130> FILE REFERENCE: 13464
14 <140> CURRENT APPLICATION NUMBER: 09/508,745
15 <141> CURRENT FILING DATE: 2000-07-12
17 <150> PRIOR APPLICATION NUMBER: PCT/AU98/00764
18 <151> PRIOR FILING DATE: 1998-09-16
20 <160> NUMBER OF SEQ ID NOS: 8
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 581
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(579)
33 <400> SEQUENCE: 1
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36  1               5                  10                  15
38 ttt gta ggt tat aag ctg agg cag aag ggt tat gtc tgt gga gct ggc    96
39 Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
40              20                  25                  30
42 ccc ggg gag ggc cca gca gct gac ccg ctg cac caa gcc atg cgg gca   144
43 Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
44          35                  40                  45
46 gct gga gat gag ttc gag acc cgc ttc cgg cgc acc ttc tct gat ctg   192
47 Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
48      50                  55                  60
50 gcg gct cag ctg cat gtg acc cca ggc tca gcc caa caa cgc ttc acc   240
51 Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
52 65                  70                  75                  80
54 cag gtc tcc gat gaa ctt ttt caa ggg ggc ccc aac tgg ggc cgc ctt   288
55 Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
56                  85                  90                  95
58 gta gcc ttc ttt gtc ttt ggg gct gca ctg tgt gct gag agt gtc aac   336
59 Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
60                 100                 105                 110
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RAW SEQUENCE LISTING   DATE: 09/08/2003
PATENT APPLICATION: **US/09/508,745** TIME: 10:42:46

·Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\09082003\I508745.raw**

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63 Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
64         115                 120                 125
66 tac ctg gag acg cgg ctg gct·gac tgg atc cac agc agt ggg ggc tgg    432
67 Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
68     130                 135                 140
70 gcg gag ttc aca gct cta tac ggg gac ggg gcc ctg gag gag gcg cgg    480
71 Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
72 145                 150                 155                 160
74 cgt ctg cgg gag ggg aac tgg gca tca gtg agg aca gtg ctg acg ggg    528
75 Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
76                 165                 170                 175
78 gcc gtg gca ctg ggg gcc ctg gta act gta ggg gcc ttt ttt gct agc    576
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89 <213> ORGANISM: Homo sapiens
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99             35                40                45
101 Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
102     50                55                  60
105 Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
106 65                  70                75                  80
108 Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
109                 85                90                  95
111 Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
112                 100                105                110
114 Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
115             115                120                125
117 Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
118     130                 135                140
120 Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
121 145                 150                 155                 160
123 Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
124                 165                170                175
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127                 180                185                190
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135 <211> LENGTH: 581
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140 <221> NAME/KEY: CDS
141 <222> LOCATION: (1)..(579)
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148 ttt gta ggc tat aag ctg agg cag aag ggt tat gtc tgt gga gct ggc    96
149 Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
150              20                  25                  30
152 cct ggg gaa ggc cca gcc gcc gac ccg ctg cac caa gcc atg cgg gct   144
153 Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
154          35                  40                  45
156 gct gga gac gag ttt gag acc cgt ttc cgc cgc acc ttc tct gac ctg   192
157 Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
158      50                  55                  60
160 gcc gct cag cta cac gtg acc cca ggc tca gcc cag caa cgc ttc acc   240
161 Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
162 65                  70                  75                  80
164 cag gtt tcc gac gaa ctt ttc caa ggg ggc cct aac tgg ggc cgt ctt   288
165 Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
166                  85                  90                  95
168 gtg gca ttc ttt gtc ttt ggg gct gcc ctg tgt gct gag agt gtc aac   336
169 Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
170              100                 105                 110
172 aaa gaa atg gag cct ttg gtg gga caa gtg cag gat tgg atg gtg gcc   384
173 Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Met Val Ala
174          115                 120                 125
176 tac ctg gag aca cgt ctg gct gac tgg atc cac agc agt ggg ggc tgg   432
177 Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
178      130                 135                 140
180 gcg gag ttc aca gct cta tac ggg gac ggg gcc ctg gag gag gca cgg   480
181 Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
182 145                 150                 155                 160
184 cgt ctg cgg gag ggg aac tgg gca tca gtg agg aca gtg ctg acg ggg   528
185 Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
186                  165                 170                 175
188 gcc gtg gca ctg ggg gcc ctg gta act gta ggg gcc ttt ttt gct agc   576
189 Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
190              180                 185                 190
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196 <210> SEQ ID NO: 4
197 <211> LENGTH: 193
198 <212> TYPE: PRT
199 <213> ORGANISM: Mus musculus
201 <400> SEQUENCE: 4
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206             20                  25                 30
209 Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
210             35                  40                 45
212 Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
213     50                  55                  60
215 Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
216 65                  70                  75                  80
218 Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
219                 85                  90                  95
221 Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
222             100                 105                 110
224 Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Met Val Ala
225             115                 120                 125
227 Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
228     130                 135                 140
230 Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
231 145                 150                 155                 160
233 Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
234                 165                 170                 175
236 Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
237             180                 185                 190
239 Lys
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244 <211> LENGTH: 583
245 <212> TYPE: DNA
246 <213> ORGANISM: Homo sapiens
248 <220> FEATURE:
249 <221> NAME/KEY: CDS
250 <222> LOCATION: (1)..(579)
252 <400> SEQUENCE: 5
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255  1               5                  10                 15
257 ttt gta ggt tat aag ctg agg cag aag ggt tat gtc tgt gga gct ggc    96
258 Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
259             20                  25                 30
261 ccc ggg gag ggc cca gca gct gac ccg ctg cac caa gcc atg cgg gca   144
262 Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
263             35                  40                 45
265 gct gga gat gag ttc gag acc cgc ttc cgg cgc acc ttc tct gat ctg   192
266 Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
267     50                  55                  60
269 gcg gct cag ctg cat gtg acc cca ggc tca gcc cag caa cgc ttc acc   240
270 Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
271 65                  70                  75                  80
273 cag gtc tcc gac gaa ctt ttt caa ggg ggc ccc aac tgg ggc cgc ctt   288
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274 Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
275                   85              ·     90                    95
277 gta gcc ttc ttt ctc ttt ggg gct gca ctg tgt gct gag agt gtc aac   336
278 Val Ala Phe Phe Leu Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
279               100                 105                 110
281 aag gag atg gaa cca ctg gtg gga caa gtg cag gag tgg atg gtg gcc   384
282 Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
283           115                 120                 125
285 tac ctg gag acg cgg ctg gtc gac tgg atc cac agc agt ggg ggc tgg   432
286 Tyr Leu Glu Thr Arg Leu Val Asp Trp Ile His Ser Ser Gly Gly Trp
287       130                 135                 140        .
289 gcg gag ttc aca gct cta tac ggg gac ggg gcc ctg gag gag gcg cgg·  480
290 Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
291 145                 150                 155                 160 .
293 cgt ctg cgg gag ggg aac tgg gca tca gtg agg aca gtg ctg acg ggg   528
294 Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
295               165                 170                 175
297 gcc gtg gca ctg ggg gcc ctg gta act gta ggg gcc ttt ttt gct agc   576
298 Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
299               180                 185                 190
301 aag tga a                     . ·                                 583
302 Lys
305 <210> SEQ ID NO: 6
306 <211> LENGTH: 193
307 <212> TYPE: PRT
308 <213> ORGANISM: Homo sapiens
310 <400> SEQUENCE: 6
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317 Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
318           35          ·       40                  45
320 Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
321       50                  55                  60
323 Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
324 65                  70                  75                  80
326 Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
327                   85                  90                  95
329 Val Ala Phe Phe Leu Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
330 .             100                 105                 110
332 Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
333           115                 120                 125
335 Tyr Leu Glu Thr Arg Leu Val Asp Trp Ile His Ser Ser Gly Gly Trp
336       130                 135                 140
338 Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
339 145                 150                 155                 160
341 Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
342               165                 170                 175
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VERIFICATION SUMMARY   DATE: 09/08/2003
PATENT APPLICATION: **US/09/508,745**   TIME: 10:42:47

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\09082003\I508745.raw**

1600

RAW SEQUENCE LISTING   DATE: 09/08/2003
PATENT APPLICATION: US/09/508,745   TIME: 10:42:16

        Input Set : A:\13464.seq.txt
        Output Set: N:\CRF4\09082003\I508745.raw

 3 <110> APPLICANT: Cory, Suzanne
 4   Adams, Jerry
 5   Print, Cris
 6   Gibson, Leonie
 7   Koentgen, Frank
 9 <120> TITLE OF INVENTION: A METHOD OF TREATMENT AND AN ANIMAL MODEL USEFUL FOR
10   SAME
12 <130> FILE REFERENCE: 13464
14 <140> CURRENT APPLICATION NUMBER: 09/508,745
15 <141> CURRENT FILING DATE: 2000-07-12
17 <150> PRIOR APPLICATION NUMBER: PCT/AU98/00764
18 <151> PRIOR FILING DATE: 1998-09-16
20 <160> NUMBER OF SEQ ID NOS: 8
22 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

417 <210> SEQ ID NO: 8
418 <211> LENGTH: 193
419 <212> TYPE: PRT
420 <213> ORGANISM: Mus musculus
422 <400> SEQUENCE: 8
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427   ·   20   25   30
429 Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
430   35   40   45
432 Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
433   50   55   60
435 Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
436 65   70   75   80
438 Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
439   85   90   95
441 Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
442   100   105   110
444 Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Ile Val Ala
445   115   120   125
447 Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
448   130   135   140
450 Ala Asp Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Asp Ala Arg
451 145   150   155   160

RAW SEQUENCE LISTING   DATE: 09/08/2003
PATENT APPLICATION: **US/09/508,745**   TIME: 10:42:16

Input Set : **A:\13464.seq.txt**
Output Set: **N:\CRF4\09082003\I508745.raw**

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  453 Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Ser Thr Val Val Thr Gly
  454             165             170             175
  456 Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
  457             180             185             190
  459 Lys
E--> 468 (1)
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VERIFICATION SUMMARY   DATE: 09/08/2003
PATENT APPLICATION: **US/09/508,745**   TIME: 10:42:17

Input Set : **A:\13464.seq.txt**
Output Set: **N:\CRF4\09082003\I508745.raw**

L:468 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8